

SEQUENCE LISTING

<110> Dhugga, Kanwarpal S.
Niu, Xiaomu
Helentjaris, Timothy

<120> Manipulation of Sucrose Synthase Genes
to Improve Stalk and Grain Quality

<130> 1301

<150> 60/270,777

<151> 2001-02-22

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2737

<212> DNA

<213> Zea mays

<400> 1

gtcgacccac gcgctcggcg accgcgtcga ggacaccctc cacgcgcacc gcaacgagct	60
cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctgcagc cgcaccacat	120
cctcgacgcg ctcgacgagg tccagggctc cgggggcccgc gcgctagccg agggaccctt	180
cctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgccgttcg tggccatcgc	240
ggtgcgcccc cgcccgggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt	300
cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgctg acggccagca	360
caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc	420
aaatcggtca tcatctattg gaaacgggtg gcagttcctc aaccgacact tgtcctcaat	480
catgttccgc aacagggatt gcttggagcc cctgttggat ttctctccgt gccaccggca	540
caaggggcat gttatgatgc ttaatgatag aatacaaagc ttggggaggc ttcagtctgt	600
gctgaccaa gctgaggagc acttgtcaaa gctccctgct gacacacat actcacaatt	660
tgtttataaa tttcaagagt ggggcctgga gaaagggttg ggtgatacag caggacatgt	720
tttgaaatg atccatctcc ttctagacat cattcaggcg ccagacccat ctaccctaga	780
gaaattcttg gggaggatcc ccatgatatt taacgttggt gtggtatccc ctcatggata	840
ctttggtcaa gctaattgat taggcttgcc agacacagga ggacagatcg tctatatact	900
ggaccaagtc cgtgcactag aaaatgagat ggttctccgt ttaaagaaac aagggcttga	960
tgtttcccca aagattctca ttgttactcg gctgatacca gatgcaaaag gaacatcatg	1020
caatcagcgg cttgagagaa ttagtggaac acagcatact tacatattac gagttccctt	1080
cagaaatgaa aatgggatac ttaagaaatg gatatcaaga tttgatgtgt ggccatatct	1140
ggaaacattt gctgaggatg ctgctggtga aattgctgct gaattacaag gtactccaga	1200
cttcataaatt ggaaactaca gtgatggaaa tcttggtggc tcattgctat cttacaagat	1260
gggaattacc cagtgaaca tgtctcatgc tctggaaaag actaagtatc cagattcaga	1320
catatttttg aagaatttcg atgagaagta ccatttctcc tgccagttca ctgctgatat	1380
aattgctatg aacaatgctg attttatcat caccagcaca taccaagaaa ttgctggaag	1440
caaaaatact gttggacagt atgagagtca tactgccttt actctgcctg gtctgtaccg	1500
agttgtccat gggatcgatg tcttcgatcc aaagttcaat atagtctctc ctggagctga	1560
catgtccata tactttccac ataccgagaa ggccaagcga ctcacctctc ttcatggttc	1620
aatcgaaaaa ttgatttatg acccgagca aaacgatgaa cacattgggc atctggatga	1680
ccggtcaaag cccatcctct tctccatggc aagactcgac aggggtgaaga acataacagg	1740
gctggctgaa gcttttgcta agtgcgctaa gctgagggag ctggtaaacc ttgtcgtcgt	1800
tgccgggtac aatgatgtca acaagtccaa ggacagggaa gagatcgcg agatagagaa	1860
gatgcatgaa ctcatcaaga cccacaactt gttcggggcag ttccgctgga tctctgccca	1920

100601.14.022402

gacaaacagg	gcccgtaacg	gcgagctcta	tcgctacatc	gctgataccc	atgggtgcttt	1980
cgtacagccg	gccttgatatg	aagcgttcgg	tctcaccgtc	gttgaggcca	tgacctgtgg	2040
gcttcctact	ttcgcgacgc	tccatggagg	tccagctgag	atcatagagc	atggcgctctc	2100
gggcttccac	attgaccctg	accaccccga	acaggctggt	aatctgatgg	ccgacttctt	2160
cgaccgggtg	aagcaagacc	cagatcactg	ggtgaatata	tctggagcag	ggctgcagcg	2220
catatacgag	aagtaacacat	ggaagatata	ctcagagagg	ttgatgacac	tggccgggggt	2280
ctacgggttc	tggaagtacg	tgtcgaagct	cgagaggctg	gagacgaggc	gctaccttga	2340
gatgttctac	atactgaagt	tccgcgagct	ggcgaagacc	gtgccgcttg	caattgacca	2400
accgcagtag	cttgcgcaac	tgcgactgcg	tagcacttgg	tacaagactg	aaacctgaag	2460
gaccttcagt	aatttaggcg	cggcagacgg	tagccaataa	aatgtgcccg	agctgaactg	2520
gttttttatt	atgtacataa	tggcagtata	acaaaattac	tgaaggcagg	tgggttgacg	2580
ttgtgtgttc	gttactgttt	actgtattat	gtcaagctgt	cggctgcaat	ttctttgctg	2640
gcaagccgca	ggcactgggtg	aagtgtctgat	aaatacatca	tattctgttg	acctgtgaaa	2700
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaagg	cggccgcg			2737

<210> 2
 <211> 802
 <212> PRT
 <213> Zea mays

<400> 2

Ser	Thr	His	Ala	Ser	Gly	Asp	Arg	Val	Glu	Asp	Thr	Leu	His	Ala	His
1				5				10						15	
Arg	Asn	Glu	Leu	Val	Ala	Leu	Leu	Ser	Lys	Tyr	Val	Asn	Lys	Gly	Lys
			20					25					30		
Gly	Ile	Leu	Gln	Pro	His	His	Ile	Leu	Asp	Ala	Leu	Asp	Glu	Val	Gln
		35					40					45			
Gly	Ser	Gly	Gly	Arg	Ala	Leu	Ala	Glu	Gly	Pro	Phe	Leu	Asp	Val	Leu
	50					55					60				
Arg	Ser	Ala	Gln	Glu	Ala	Ile	Val	Leu	Pro	Pro	Phe	Val	Ala	Ile	Ala
65				70						75				80	
Val	Arg	Pro	Arg	Pro	Gly	Val	Trp	Glu	Tyr	Val	Arg	Val	Asn	Val	His
			85					90					95		
Glu	Leu	Ser	Val	Glu	Gln	Leu	Thr	Val	Ser	Glu	Tyr	Leu	Arg	Phe	Lys
		100						105					110		
Glu	Glu	Leu	Val	Asp	Gly	Gln	His	Asn	Asp	Pro	Tyr	Val	Leu	Glu	Leu
		115					120					125			
Asp	Phe	Glu	Pro	Phe	Asn	Val	Ser	Val	Pro	Arg	Pro	Asn	Arg	Ser	Ser
	130					135				140					
Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu	Asn	Arg	His	Leu	Ser	Ser	Ile
145				150					155					160	
Met	Phe	Arg	Asn	Arg	Asp	Cys	Leu	Glu	Pro	Leu	Leu	Asp	Phe	Leu	Arg
			165					170						175	
Gly	His	Arg	His	Lys	Gly	His	Val	Met	Met	Leu	Asn	Asp	Arg	Ile	Gln
		180						185					190		
Ser	Leu	Gly	Arg	Leu	Gln	Ser	Val	Leu	Thr	Lys	Ala	Glu	Glu	His	Leu
	195						200					205			
Ser	Lys	Leu	Pro	Ala	Asp	Thr	Pro	Tyr	Ser	Gln	Phe	Ala	Tyr	Lys	Phe
	210					215					220				
Gln	Glu	Trp	Gly	Leu	Glu	Lys	Gly	Trp	Gly	Asp	Thr	Ala	Gly	His	Val
225				230						235				240	
Leu	Glu	Met	Ile	His	Leu	Leu	Leu	Asp	Ile	Ile	Gln	Ala	Pro	Asp	Pro
			245					250						255	
Ser	Thr	Leu	Glu	Lys	Phe	Leu	Gly	Arg	Ile	Pro	Met	Ile	Phe	Asn	Val
		260					265					270			
Val	Val	Val	Ser	Pro	His	Gly	Tyr	Phe	Gly	Gln	Ala	Asn	Val	Leu	Gly
	275					280					285				
Leu	Pro	Asp	Thr	Gly	Gly	Gln	Ile	Val	Tyr	Ile	Leu	Asp	Gln	Val	Arg

10030114-022102

290	295	300
Ala Leu Glu Asn Glu Met Val Leu Arg Leu Lys Lys Gln Gly Leu Asp		
305	310	315
Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys		
	325	330
Gly Thr Ser Cys Asn Gln Arg Leu Glu Arg Ile Ser Gly Thr Gln His		
	340	345
Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys		
	355	360
Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala		
	370	375
Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro Asp		
385	390	395
Phe Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu		
	405	410
Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His Ala Leu Glu		
	420	425
Lys Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu		
	435	440
Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Ile Ile Ala Met Asn		
	450	455
Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser		
465	470	475
Lys Asn Thr Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro		
	485	490
Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe		
	500	505
Asn Ile Val Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro His Thr		
	515	520
Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu		
	530	535
Ile Tyr Asp Pro Glu Gln Asn Asp Glu His Ile Gly His Leu Asp Asp		
545	550	555
Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg Val Lys		
	565	570
Asn Ile Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg		
	580	585
Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn Asp Val Asn Lys		
	595	600
Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu		
	610	615
Ile Lys Thr His Asn Leu Phe Gly Gln Phe Arg Trp Ile Ser Ala Gln		
625	630	635
Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr		
	645	650
His Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr		
	660	665
Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His		
	675	680
Gly Gly Pro Ala Glu Ile Ile Glu His Gly Val Ser Gly Phe His Ile		
	690	695
Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe Phe		
705	710	715
Asp Arg Cys Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala		
	725	730
Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile Tyr Ser Glu		
	740	745
Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser		

10080114-022102

755	760	765
Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu Glu Met Phe Tyr Ile		
770	775	780
Leu Lys Phe Arg Glu Leu Ala Lys Thr Val Pro Leu Ala Ile Asp Gln		
785	790	795
Pro Gln		800

<210> 3
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon the adapter
 sequence and poly T to remove clones which have a
 poly A tail but no cDNA.

<400> 3
 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa 36

<210> 4
 <211> 2746
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (72)...(2480)

<400> 4
 aaaccctccc tccctcctcc attggactgc ttgctccctg ttgaccattg ggtattctga 60
 accatcgagc c atg gct gcc aag ctg act cgc ctt cac agt ctt cgc gaa 110
 Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu
 1 5 10
 cgc ctt ggt gcc acc ttc tcc tcc cat ccc aat gaa ctg ata gca ctc 158
 Arg Leu Gly Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu
 15 20 25
 ttt tcc agg tat gtt cac cag ggc aag gga atg ctt cag cgc cat cag 206
 Phe Ser Arg Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln
 30 35 40 45
 ctg ctt gcg gag ttt gat gcc ctg ttt gat agt gac aag gag aag tat 254
 Leu Leu Ala Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr
 50 55 60
 gca cca ttt gaa gac att ctt cgt gct gct cag gaa gca att gtg ctc 302
 Ala Pro Phe Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu
 65 70 75
 ccc cca tgg gtt gca ctt gct atc agg cca agg cct ggt gtc tgg gat 350
 Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp
 80 85 90
 tac att cgg gtg aat gta agt gag ctg gct gtg gag gag ctg agt gtt 398

10080114-022102

Tyr	Ile	Arg	Val	Asn	Val	Ser	Glu	Leu	Ala	Val	Glu	Glu	Leu	Ser	Val		
95						100					105						
tct	gag	tac	ttg	gca	ttc	aag	gaa	cag	ctg	gtg	gat	gga	caa	tcc	aac	446	
Ser	Glu	Tyr	Leu	Ala	Phe	Lys	Glu	Gln	Leu	Val	Asp	Gly	Gln	Ser	Asn		
110					115					120					125		
agc	aac	ttt	gtg	ctt	gag	ctt	gat	ttt	gag	ccc	ttc	aat	gcc	tcc	ttt	494	
Ser	Asn	Phe	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ala	Ser	Phe		
				130					135					140			
cct	cgt	cct	tcc	atg	tcg	aag	tcc	atc	gga	aat	gga	gtg	caa	ttc	ctt	542	
Pro	Arg	Pro	Ser	Met	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu		
			145					150					155				
aac	cga	cac	ctg	tcg	tcc	aag	ttg	ttc	cag	gac	aag	gag	agt	ttg	tac	590	
Asn	Arg	His	Leu	Ser	Ser	Lys	Leu	Phe	Gln	Asp	Lys	Glu	Ser	Leu	Tyr		
		160					165					170					
ccc	ttg	ctg	aac	ttc	ctc	aag	gct	cat	aac	tac	aag	ggc	acg	acg	atg	638	
Pro	Leu	Leu	Asn	Phe	Leu	Lys	Ala	His	Asn	Tyr	Lys	Gly	Thr	Thr	Met		
	175					180					185						
atg	ttg	aat	gac	aga	atc	caa	agc	ctt	cgt	ggt	ctc	caa	tca	tcc	ctg	686	
Met	Leu	Asn	Asp	Arg	Ile	Gln	Ser	Leu	Arg	Gly	Leu	Gln	Ser	Ser	Leu		
190					195				200						205		
aga	aag	gca	gag	gag	tat	cta	ctg	agt	gtt	cct	caa	gac	act	ccc	tac	734	
Arg	Lys	Ala	Glu	Glu	Tyr	Leu	Leu	Ser	Val	Pro	Gln	Asp	Thr	Pro	Tyr		
				210					215					220			
tcg	gag	ttc	aac	cat	agg	ttc	caa	gag	ctt	ggc	ttg	gag	aag	ggt	tgg	782	
Ser	Glu	Phe	Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp		
			225				230						235				
ggt	gac	act	gcg	aag	cgt	gtt	ctc	gac	aca	ctc	cac	ttg	ctt	ctc	gac	830	
Gly	Asp	Thr	Ala	Lys	Arg	Val	Leu	Asp	Thr	Leu	His	Leu	Leu	Leu	Asp		
		240				245					250						
ctt	ctt	gag	gcc	cct	gat	cct	gcc	aac	ttg	gag	aag	ttc	ctt	gga	act	878	
Leu	Leu	Glu	Ala	Pro	Asp	Pro	Ala	Asn	Leu	Glu	Lys	Phe	Leu	Gly	Thr		
	255					260					265						
ata	cca	atg	atg	ttc	aac	gtt	gtt	atc	ctg	tct	cct	cat	ggc	tac	ttc	926	
Ile	Pro	Met	Met	Phe	Asn	Val	Val	Ile	Leu	Ser	Pro	His	Gly	Tyr	Phe		
270					275				280						285		
gcc	cag	tcc	aat	gtg	ctt	gga	tac	cct	gac	act	ggc	ggt	cag	gtt	gtg	974	
Ala	Gln	Ser	Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val		
				290					295					300			
tac	att	ctg	gat	caa	gtc	cgt	gct	ttg	gag	aat	gag	atg	ctt	ctg	agg	1022	
Tyr	Ile	Leu	Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg		
			305					310					315				
att	aag	cag	caa	ggc	ctt	gat	atc	act	ccg	aag	atc	ctc	att	gtt	acc	1070	
Ile	Lys	Gln	Gln	Gly	Leu	Asp	Ile	Thr	Pro	Lys	Ile	Leu	Ile	Val	Thr		
		320				325						330					

10050114-022102

agg ctg ttg cct gat gct gct ggg act acg tgc ggt cag cgg ctg gag Arg Leu Leu Pro Asp Ala Ala Gly Thr Thr Cys Gly Gln Arg Leu Glu 335 340 345	1118
aag gtc att ggt act gag cac aca gac atc att cgc gtt ccc ttc aga Lys Val Ile Gly Thr Glu His Thr Asp Ile Ile Arg Val Pro Phe Arg 350 355 360 365	1166
aat gag aat ggc atc ctc cgc aag tgg atc tct cgt ttt gat gtc tgg Asn Glu Asn Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp 370 375 380	1214
cca tac ctg gag aca tac act gag gat gtt tcc agt gaa ata atg aaa Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ser Ser Glu Ile Met Lys 385 390 395	1262
gaa atg cag gcc aag cct gac ctt atc att ggc aac tac agc gat ggc Glu Met Gln Ala Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly 400 405 410	1310
aac cta gtc gcc act ctg ctc gcg cac aag ttg gga gtc act cag tgt Asn Leu Val Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys 415 420 425	1358
acc atc gct cat gcc ttg gag aaa acc aaa tac ccc aac tcg gac atc Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile 430 435 440 445	1406
tac ttg gac aaa ttc gac agc cag tac cac ttc tct tgc cag ttc aca Tyr Leu Asp Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr 450 455 460	1454
gct gac ctt att gcc atg aac cac acc gat ttc atc atc acc agc aca Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr 465 470 475	1502
ttc caa gaa atc gcg gga agc aag gac acc gtg ggg cag tac gag tcc Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser 480 485 490	1550
cat atc gcg ttc act ctt cct ggg ctc tac cgt gtc gtc cat ggc atc His Ile Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile 495 500 505	1598
gat gtt ttc gat ccc aag ttc aac att gtc tct cct gga gca gac atg Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met 510 515 520 525	1646
agt gtt tac tac cct tat acg gaa acc gac aag aga ctc act gcc ttc Ser Val Tyr Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe 530 535 540	1694
cat cct gaa atc gag gag ctc atc tac agc gac gtc gag aac tcc gag His Pro Glu Ile Glu Glu Leu Ile Tyr Ser Asp Val Glu Asn Ser Glu 545 550 555	1742
cac aag ttc gtg ctg aag gac aag aag aag ccg atc atc ttc tcg atg	1790

His	Lys	Phe	Val	Leu	Lys	Asp	Lys	Lys	Lys	Pro	Ile	Ile	Phe	Ser	Met		
		560					565					570					
gcg	cgt	ctc	gac	cgc	gtg	aag	aac	atg	aca	ggc	ctg	gtc	gag	atg	tac	1838	
Ala	Arg	Leu	Asp	Arg	Val	Lys	Asn	Met	Thr	Gly	Leu	Val	Glu	Met	Tyr		
	575					580					585						
ggc	aag	aac	gcg	cgc	ctg	agg	gag	ctg	gcg	aac	ctc	gtg	atc	gtt	gcc	1886	
Gly	Lys	Asn	Ala	Arg	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Val	Ile	Val	Ala		
590					595					600					605		
ggg	gac	cac	ggc	aag	gag	tcc	aag	gac	agg	gag	gag	cag	gag	gtt	gtc	1934	
Gly	Asp	His	Gly	Lys	Glu	Ser	Lys	Asp	Arg	Glu	Glu	Gln	Ala	Glu	Phe		
			610						615					620			
aag	aag	atg	tac	agc	ctc	atc	gac	gag	tac	aag	ttg	aag	ggc	cat	atc	1982	
Lys	Lys	Met	Tyr	Ser	Leu	Ile	Asp	Glu	Tyr	Lys	Leu	Lys	Gly	His	Ile		
			625					630					635				
cgg	tgg	atc	tcg	gcg	cag	atg	aac	cgt	gtc	cgc	aac	ggg	gag	ctg	tac	2030	
Arg	Trp	Ile	Ser	Ala	Gln	Met	Asn	Arg	Val	Arg	Asn	Gly	Glu	Leu	Tyr		
		640					645					650					
cgc	tac	att	tgc	gat	acc	aag	ggc	gca	ttc	gtg	cag	cct	gag	ttc	tac	2078	
Arg	Tyr	Ile	Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val	Gln	Pro	Ala	Phe	Tyr		
	655					660					665						
gaa	gag	ttc	ggc	ctg	act	gtg	atc	gag	tcc	atg	acg	tgc	ggg	ctg	cca	2126	
Glu	Ala	Phe	Gly	Leu	Thr	Val	Ile	Glu	Ser	Met	Thr	Cys	Gly	Leu	Pro		
670					675					680					685		
acg	atc	gag	acc	tgc	cat	ggc	ggc	cct	gct	gag	atc	atc	gtg	gac	ggg	2174	
Thr	Ile	Ala	Thr	Cys	His	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Val	Asp	Gly		
				690					695					700			
gta	tct	ggc	ctg	cac	att	gac	cct	tac	cac	agc	gac	aag	gcc	gag	gat	2222	
Val	Ser	Gly	Leu	His	Ile	Asp	Pro	Tyr	His	Ser	Asp	Lys	Ala	Ala	Asp		
			705					710					715				
atc	ctg	gtc	aac	ttc	ttt	gac	aaa	tgc	aag	gca	gat	ccg	agc	tac	tgg	2270	
Ile	Leu	Val	Asn	Phe	Phe	Asp	Lys	Cys	Lys	Ala	Asp	Pro	Ser	Tyr	Trp		
		720					725					730					
gac	gag	atc	tca	cag	ggc	ggc	ctg	cag	aga	att	tat	gag	aag	tac	acc	2318	
Asp	Glu	Ile	Ser	Gln	Gly	Gly	Leu	Gln	Arg	Ile	Tyr	Glu	Lys	Tyr	Thr		
	735					740					745						
tgg	aag	ctc	tac	tcc	gag	agg	ctg	atg	acc	ctg	acc	ggc	gtg	tac	ggg	2366	
Trp	Lys	Leu	Tyr	Ser	Glu	Arg	Leu	Met	Thr	Leu	Thr	Gly	Val	Tyr	Gly		
750					755					760					765		
ttc	tgg	aag	tac	gtg	agc	aac	ctg	gag	agg	cgc	gag	acc	cgc	cgc	tac	2414	
Phe	Trp	Lys	Tyr	Val	Ser	Asn	Leu	Glu	Arg	Arg	Glu	Thr	Arg	Arg	Tyr		
				770				775						780			
atc	gag	atg	ttc	tac	gcc	ctg	aag	tac	cgt	agc	ctg	gca	agc	cag	gtt	2462	
Ile	Glu	Met	Phe	Tyr	Ala	Leu	Lys	Tyr	Arg	Ser	Leu	Ala	Ser	Gln	Val		
			785					790						795			

ccg ctg tcc ttc gat tag tacggggaaa gaaggagaag aagaagaaga 2510
 Pro Leu Ser Phe Asp *
 800

agcccaggcc ggagaaccat cgcttgcat tcatctgtt tcaccgcaat tcgcattggt 2570
 agtcgtgtat tggagttatg tgtacttggg ttccaagaac tttgggttcct tctcgttttt 2630
 tttccttggt tgagcgtttt tgggcagcgc tggcctgggt cctagtatgg tgggaattgg 2690
 ctgcaccttt tgcttcgaat aaaaatgcct gctcgttcac ctgtcttcca gagtgc 2746

<210> 5
 <211> 802
 <212> PRT
 <213> Zea mays

<400> 5
 Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
 1 5 10 15
 Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Arg
 20 25 30
 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Ala
 35 40 45
 Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr Ala Pro Phe
 50 55 60
 Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
 65 70 75 80
 Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
 85 90 95
 Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val Ser Glu Tyr
 100 105 110
 Leu Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn Ser Asn Phe
 115 120 125
 Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
 130 135 140
 Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
 145 150 155 160
 Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
 165 170 175
 Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met Met Leu Asn
 180 185 190
 Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ser Leu Arg Lys Ala
 195 200 205
 Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr Ser Glu Phe
 210 215 220
 Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
 225 230 235 240
 Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp Leu Leu Glu
 245 250 255
 Ala Pro Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
 260 265 270
 Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
 275 280 285
 Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
 290 295 300
 Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
 305 310 315 320
 Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
 325 330 335

1003014.022102

Pro	Asp	Ala	Ala	Gly	Thr	Thr	Cys	Gly	Gln	Arg	Leu	Glu	Lys	Val	Ile
			340					345					350		
Gly	Thr	Glu	His	Thr	Asp	Ile	Ile	Arg	Val	Pro	Phe	Arg	Asn	Glu	Asn
		355					360					365			
Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu
	370					375					380				
Glu	Thr	Tyr	Thr	Glu	Asp	Val	Ser	Ser	Glu	Ile	Met	Lys	Glu	Met	Gln
385					390					395					400
Ala	Lys	Pro	Asp	Leu	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val
				405				410						415	
Ala	Thr	Leu	Leu	Ala	His	Lys	Leu	Gly	Val	Thr	Gln	Cys	Thr	Ile	Ala
			420					425						430	
His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr	Pro	Asn	Ser	Asp	Ile	Tyr	Leu	Asp
		435					440					445			
Lys	Phe	Asp	Ser	Gln	Tyr	His	Phe	Ser	Cys	Gln	Phe	Thr	Ala	Asp	Leu
	450					455					460				
Ile	Ala	Met	Asn	His	Thr	Asp	Phe	Ile	Ile	Thr	Ser	Thr	Phe	Gln	Glu
465					470					475					480
Ile	Ala	Gly	Ser	Lys	Asp	Thr	Val	Gly	Gln	Tyr	Glu	Ser	His	Ile	Ala
				485				490						495	
Phe	Thr	Leu	Pro	Gly	Leu	Tyr	Arg	Val	Val	His	Gly	Ile	Asp	Val	Phe
			500					505					510		
Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met	Ser	Val	Tyr
		515					520					525			
Tyr	Pro	Tyr	Thr	Glu	Thr	Asp	Lys	Arg	Leu	Thr	Ala	Phe	His	Pro	Glu
	530					535					540				
Ile	Glu	Glu	Leu	Ile	Tyr	Ser	Asp	Val	Glu	Asn	Ser	Glu	His	Lys	Phe
545					550					555					560
Val	Leu	Lys	Asp	Lys	Lys	Lys	Pro	Ile	Ile	Phe	Ser	Met	Ala	Arg	Leu
				565					570					575	
Asp	Arg	Val	Lys	Asn	Met	Thr	Gly	Leu	Val	Glu	Met	Tyr	Gly	Lys	Asn
			580				585						590		
Ala	Arg	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Val	Ile	Val	Ala	Gly	Asp	His
		595					600					605			
Gly	Lys	Glu	Ser	Lys	Asp	Arg	Glu	Glu	Gln	Ala	Glu	Phe	Lys	Lys	Met
	610					615					620				
Tyr	Ser	Leu	Ile	Asp	Glu	Tyr	Lys	Leu	Lys	Gly	His	Ile	Arg	Trp	Ile
625					630					635					640
Ser	Ala	Gln	Met	Asn	Arg	Val	Arg	Asn	Gly	Glu	Leu	Tyr	Arg	Tyr	Ile
				645					650					655	
Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val	Gln	Pro	Ala	Phe	Tyr	Glu	Ala	Phe
			660				665						670		
Gly	Leu	Thr	Val	Ile	Glu	Ser	Met	Thr	Cys	Gly	Leu	Pro	Thr	Ile	Ala
	675						680					685			
Thr	Cys	His	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Val	Asp	Gly	Val	Ser	Gly
	690					695					700				
Leu	His	Ile	Asp	Pro	Tyr	His	Ser	Asp	Lys	Ala	Ala	Asp	Ile	Leu	Val
705					710					715					720
Asn	Phe	Phe	Asp	Lys	Cys	Lys	Ala	Asp	Pro	Ser	Tyr	Trp	Asp	Glu	Ile
				725					730					735	
Ser	Gln	Gly	Gly	Leu	Gln	Arg	Ile	Tyr	Glu	Lys	Tyr	Thr	Trp	Lys	Leu
			740					745					750		
Tyr	Ser	Glu	Arg	Leu	Met	Thr	Leu	Thr	Gly	Val	Tyr	Gly	Phe	Trp	Lys
		755					760					765			
Tyr	Val	Ser	Asn	Leu	Glu	Arg	Arg	Glu	Thr	Arg	Arg	Tyr	Ile	Glu	Met
	770					775					780				
Phe	Tyr	Ala	Leu	Lys	Tyr	Arg	Ser	Leu	Ala	Ser	Gln	Val	Pro	Leu	Ser
785					790					795					800

10080114-022402

Phe Asp

<210> 6
<211> 2908
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (28) ... (2478)

<400> 6
gcctgaggat ccaggaagag gacagca atg ggg gaa ggt gca ggt gac cgt gtc 54
Met Gly Glu Gly Ala Gly Asp Arg Val
1 5

ctg agc cgc ctc cac agc gtc agg gag cgc att ggc gac tca ctc tct 102
Leu Ser Arg Leu His Ser Val Arg Glu Arg Ile Gly Asp Ser Leu Ser
10 15 20 25

gcc cac ccc aat gag ctt gtc gcc gtc ttc acc agg ctg aaa aac ctt 150
Ala His Pro Asn Glu Leu Val Ala Val Phe Thr Arg Leu Lys Asn Leu
30 35 40

gga aag ggt atg ctg cag ccc cac cag atc att gcc gag tac aac aat 198
Gly Lys Gly Met Leu Gln Pro His Gln Ile Ile Ala Glu Tyr Asn Asn
45 50 55

gcg atc cct gag gct gag cgc gag aag ctc aag gat ggt gct ttt gag 246
Ala Ile Pro Glu Ala Glu Arg Glu Lys Leu Lys Asp Gly Ala Phe Glu
60 65 70

gat gtc ctg agg gca gct cag gag gcg att gtc atc ccc cca tgg gtt 294
Asp Val Leu Arg Ala Ala Gln Glu Ala Ile Val Ile Pro Pro Trp Val
75 80 85

gca ctt gcc atc cgc cct agg cct ggt gtc tgg gag tat gtg agg gtc 342
Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val
90 95 100 105

aac gtc agt gag ctc gct gtt gag gag ctg aga gtt cct gag tac ctg 390
Asn Val Ser Glu Leu Ala Val Glu Glu Leu Arg Val Pro Glu Tyr Leu
110 115 120

cag ttc aag gaa cag ctt gtg gaa gaa ggc ccc aac aac aac ttt gtt 438
Gln Phe Lys Glu Gln Leu Val Glu Glu Gly Pro Asn Asn Asn Phe Val
125 130 135

ctt gag ctg gac ttt gag cca ttc aat gcc tcc ttc ccc cgt cct tct 486
Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro Ser
140 145 150

ctg tca aag tcc att ggc aat ggc gtg cag ttc ctc aac agg cac ctg 534
Leu Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu
155 160 165

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

tca tca aag ctc ttc cat gac aag gag agc atg tac ccc ttg ctc aac	582
Ser Ser Lys Leu Phe His Asp Lys Glu Ser Met Tyr Pro Leu Leu Asn	
170 175 180 185	
ttc ctt cgc gcc cac aac tac aag ggg atg acc atg atg ttg aac gac	630
Phe Leu Arg Ala His Asn Tyr Lys Gly Met Thr Met Met Leu Asn Asp	
190 195 200	
aga atc cgc agt ctc agt gct ctg caa ggt gcg ctg agg aag gct gag	678
Arg Ile Arg Ser Leu Ser Ala Leu Gln Gly Ala Leu Arg Lys Ala Glu	
205 210 215	
gag cac ctg tcc acc cta caa gct gat acc cca tac tct gaa ttt cac	726
Glu His Leu Ser Thr Leu Gln Ala Asp Thr Pro Tyr Ser Glu Phe His	
220 225 230	
cac agg ttc cag gaa ctt ggt ctg gag aag ggt tgg ggt gat tgc gct	774
His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Cys Ala	
235 240 245	
aag cgt gca cag gag act atc cac ctc ctc ttg gac ctc ctg gag gcc	822
Lys Arg Ala Gln Glu Thr Ile His Leu Leu Leu Asp Leu Leu Glu Ala	
250 255 260 265	
cca gat ccg tcc acc ctg gag aag ttc ctt gga acg atc ccc atg gtg	870
Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Thr Ile Pro Met Val	
270 275 280	
ttc aat gtc gtt atc ctc tcc cct cat ggt tac ttc gct caa gct aat	918
Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ala Asn	
285 290 295	
gtc ttg ggt tac cct gac acc gga ggc cag gtt gtc tac atc ttg gat	966
Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu Asp	
300 305 310	
caa gtg cgc gct atg gag aac gaa atg ctg ctg agg atc aag cag tgt	1014
Gln Val Arg Ala Met Glu Asn Glu Met Leu Leu Arg Ile Lys Gln Cys	
315 320 325	
ggg ctt gac atc acg ccg aag atc ctt att gtc acc agg ttg ctc cct	1062
Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu Pro	
330 335 340 345	
gat gca act ggc acc acc tgt ggc cag cgc ctt gag aag gtc ctt ggc	1110
Asp Ala Thr Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Leu Gly	
350 355 360	
acc gag cac tgc cat atc ctt cgc gtg cca ttc aga aca gaa aac gga	1158
Thr Glu His Cys His Ile Leu Arg Val Pro Phe Arg Thr Glu Asn Gly	
365 370 375	
atc gtt cgc aag tgg atc tcg cga ttt gaa gtc tgg ccg tac ctg gag	1206
Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Val Trp Pro Tyr Leu Glu	
380 385 390	
act tac act gat gac gtg gcg cat gag att gct gga gag ctt cag gcc	1254
Thr Tyr Thr Asp Asp Val Ala His Glu Ile Ala Gly Glu Leu Gln Ala	

395	400	405	
aat cct gac ctg atc atc gga aac tac agt gac gga aac ctt gtt gcg Asn Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala 410 415 420 425			1302
tgt ttg ctc gcc cac aag atg ggt gtt act cac tgt acc att gcc cat Cys Leu Leu Ala His Lys Met Gly Val Thr His Cys Thr Ile Ala His 430 435 440			1350
gcg ctt gag aaa act aag tac cct aac tcc gac ctc tac tgg aag aag Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Leu Tyr Trp Lys Lys 445 450 455			1398
ttt gag gat cac tac cac ttc tcg tgc cag ttc acc act gac ttg att Phe Glu Asp His Tyr His Phe Ser Cys Gln Phe Thr Thr Asp Leu Ile 460 465 470			1446
gca atg aac cat gcc gac ttc atc atc acc agt acc ttc caa gag atc Ala Met Asn His Ala Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu Ile 475 480 485			1494
gcc gga aac aag gac acc gtc ggc cag tac gag tca cac atg gcg ttc Ala Gly Asn Lys Asp Thr Val Gly Gln Tyr Glu Ser His Met Ala Phe 490 495 500 505			1542
aca atg cct ggc ctg tac cgc gtt gtc cac ggc att gat gtg ttc gac Thr Met Pro Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp 510 515 520			1590
ccc aag ttc aac atc gtg tct cct ggc gcg gac ctg tcc atc tac ttc Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Leu Ser Ile Tyr Phe 525 530 535			1638
ccg tac acc gag tcg cac aag agg ctg acc tcc ctt cac ccg gag att Pro Tyr Thr Glu Ser His Lys Arg Leu Thr Ser Leu His Pro Glu Ile 540 545 550			1686
gag gag ctc ctg tac agc caa acc gag aac acg gag cac aag ttc gtt Glu Glu Leu Leu Tyr Ser Gln Thr Glu Asn Thr Glu His Lys Phe Val 555 560 565			1734
ctg aac gac agg aac aag cca atc atc ttc tcc atg gct cgt ctc gac Leu Asn Asp Arg Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu Asp 570 575 580 585			1782
cgt gtg aag aac ttg act ggg ctg gtg gag ctg tac ggc cgg aac aag Arg Val Lys Asn Leu Thr Gly Leu Val Glu Leu Tyr Gly Arg Asn Lys 590 595 600			1830
cgg ctg cag gag ctg gtg aac ctc gtg gtc gtc tgc ggc gac cat ggc Arg Leu Gln Glu Leu Val Asn Leu Val Val Val Cys Gly Asp His Gly 605 610 615			1878
aac cct tcc aag gac aag gag gag cag gcc gag ttc aag aag atg ttt Asn Pro Ser Lys Asp Lys Glu Glu Gln Ala Glu Phe Lys Lys Met Phe 620 625 630			1926

gac ctc atc gag cag tac aac ctg aac ggg cac atc cgc tgg atc tcc Asp Leu Ile Glu Gln Tyr Asn Leu Asn Gly His Ile Arg Trp Ile Ser 635 640 645	1974
gcc cag atg aac cgc gtc cgc aac ggc gag ctg tac cgc tac atc tgc Ala Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Cys 650 655 660 665	2022
gac acc aag ggc gcc ttc gtg cag cct gct ttc tac gag gct ttc ggg Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe Gly 670 675 680	2070
ctg acg gtg gtt gag gcc atg acc tgc ggc ctg ccc acg ttc gcc acc Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr 685 690 695	2118
gcc tac ggc ggt ccg gcc gag atc atc gtg cac ggc gtg tct ggc tac Ala Tyr Gly Gly Pro Ala Glu Ile Ile Val His Gly Val Ser Gly Tyr 700 705 710	2166
cac atc gac cct tac cag ggc gac aag gcg tcg gcc ctg ctc gtg gac His Ile Asp Pro Tyr Gln Gly Asp Lys Ala Ser Ala Leu Leu Val Asp 715 720 725	2214
ttc ttc gac aag tgc cag gcg gag ccg agc cac tgg agc aag atc tcc Phe Phe Asp Lys Cys Gln Ala Glu Pro Ser His Trp Ser Lys Ile Ser 730 735 740 745	2262
cag ggc ggg ctc cag cgt atc gag gag aag tac acc tgg aag ctg tac Gln Gly Gly Leu Gln Arg Ile Glu Glu Lys Tyr Thr Trp Lys Leu Tyr 750 755 760	2310
tcg gag agg ctg atg acc ctc acc ggc gtg tac ggg ttc tgg aag tac Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys Tyr 765 770 775	2358
gtg tcc aac ctg gag agg cgc gag acc cgg cgg tac ctg gag atg ctg Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met Leu 780 785 790	2406
tac gcg ctc aag tac cgc acc atg gcg agc acc gtg ccg ctg gcc gtg Tyr Ala Leu Lys Tyr Arg Thr Met Ala Ser Thr Val Pro Leu Ala Val 795 800 805	2454
gag gga gag ccc tcc agc aag tga tgcgtgacgg cggccacaga cctgatcgat Glu Gly Glu Pro Ser Ser Lys * 810 815	2508
cgatgagcga gagggagcac tcggagtgtc gtgtcttttc ccttgccatt tctttctttc ttctttttcc ttcccggagg cgaaaaaaaa agagtctgct tttgctaggc ggcgggcggt cgttgctgct ctttgcttca agagttaaaa ttacctacc ttgtcaaggc cttgttccat cattgatccg ggtgtcgctt gtagtagtct gatggactgt tagtagtttg cgttgcgctcg gttgagaggg aacgttggtg gtggtggtgt gtgtgcagtc aggcgtggtg ctccctttgt ttcctggatg ggatgttgct ccttgaataa taatcgtagt ggccttgag cccttttcct gaaataagag cagcatccta gtgcttacct ttgcagctgt	2568 2628 2688 2748 2808 2868 2908
<210> 7	
<211> 816	

<212> PRT
 <213> Zea mays

<400> 7

Met	Gly	Glu	Gly	Ala	Gly	Asp	Arg	Val	Leu	Ser	Arg	Leu	His	Ser	Val
1				5				10					15		
Arg	Glu	Arg	Ile	Gly	Asp	Ser	Leu	Ser	Ala	His	Pro	Asn	Glu	Leu	Val
			20					25					30		
Ala	Val	Phe	Thr	Arg	Leu	Lys	Asn	Leu	Gly	Lys	Gly	Met	Leu	Gln	Pro
		35					40					45			
His	Gln	Ile	Ile	Ala	Glu	Tyr	Asn	Asn	Ala	Ile	Pro	Glu	Ala	Glu	Arg
		50				55					60				
Glu	Lys	Leu	Lys	Asp	Gly	Ala	Phe	Glu	Asp	Val	Leu	Arg	Ala	Ala	Gln
65					70					75					80
Glu	Ala	Ile	Val	Ile	Pro	Pro	Trp	Val	Ala	Leu	Ala	Ile	Arg	Pro	Arg
				85					90					95	
Pro	Gly	Val	Trp	Glu	Tyr	Val	Arg	Val	Asn	Val	Ser	Glu	Leu	Ala	Val
			100					105					110		
Glu	Glu	Leu	Arg	Val	Pro	Glu	Tyr	Leu	Gln	Phe	Lys	Glu	Gln	Leu	Val
		115					120					125			
Glu	Glu	Gly	Pro	Asn	Asn	Asn	Phe	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro
		130				135						140			
Phe	Asn	Ala	Ser	Phe	Pro	Arg	Pro	Ser	Leu	Ser	Lys	Ser	Ile	Gly	Asn
145					150					155					160
Gly	Val	Gln	Phe	Leu	Asn	Arg	His	Leu	Ser	Ser	Lys	Leu	Phe	His	Asp
				165					170					175	
Lys	Glu	Ser	Met	Tyr	Pro	Leu	Leu	Asn	Phe	Leu	Arg	Ala	His	Asn	Tyr
			180					185					190		
Lys	Gly	Met	Thr	Met	Met	Leu	Asn	Asp	Arg	Ile	Arg	Ser	Leu	Ser	Ala
		195					200					205			
Leu	Gln	Gly	Ala	Leu	Arg	Lys	Ala	Glu	Glu	His	Leu	Ser	Thr	Leu	Gln
		210				215					220				
Ala	Asp	Thr	Pro	Tyr	Ser	Glu	Phe	His	His	Arg	Phe	Gln	Glu	Leu	Gly
225					230					235					240
Leu	Glu	Lys	Gly	Trp	Gly	Asp	Cys	Ala	Lys	Arg	Ala	Gln	Glu	Thr	Ile
				245					250					255	
His	Leu	Leu	Leu	Asp	Leu	Leu	Glu	Ala	Pro	Asp	Pro	Ser	Thr	Leu	Glu
			260				265						270		
Lys	Phe	Leu	Gly	Thr	Ile	Pro	Met	Val	Phe	Asn	Val	Val	Ile	Leu	Ser
		275				280						285			
Pro	His	Gly	Tyr	Phe	Ala	Gln	Ala	Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr
		290			295						300				
Gly	Gly	Gln	Val	Val	Tyr	Ile	Leu	Asp	Gln	Val	Arg	Ala	Met	Glu	Asn
305					310					315					320
Glu	Met	Leu	Leu	Arg	Ile	Lys	Gln	Cys	Gly	Leu	Asp	Ile	Thr	Pro	Lys
				325					330					335	
Ile	Leu	Ile	Val	Thr	Arg	Leu	Leu	Pro	Asp	Ala	Thr	Gly	Thr	Thr	Cys
			340					345					350		
Gly	Gln	Arg	Leu	Glu	Lys	Val	Leu	Gly	Thr	Glu	His	Cys	His	Ile	Leu
		355				360						365			
Arg	Val	Pro	Phe	Arg	Thr	Glu	Asn	Gly	Ile	Val	Arg	Lys	Trp	Ile	Ser
		370				375						380			
Arg	Phe	Glu	Val	Trp	Pro	Tyr	Leu	Glu	Thr	Tyr	Thr	Asp	Asp	Val	Ala
385					390					395					400
His	Glu	Ile	Ala	Gly	Glu	Leu	Gln	Ala	Asn	Pro	Asp	Leu	Ile	Ile	Gly
			405						410					415	
Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val	Ala	Cys	Leu	Leu	Ala	His	Lys	Met
			420					425					430		

1008014-02402

Gly	Val	Thr	His	Cys	Thr	Ile	Ala	His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr		
		435					440					445					
Pro	Asn	Ser	Asp	Leu	Tyr	Trp	Lys	Lys	Phe	Glu	Asp	His	Tyr	His	Phe		
		450					455					460					
Ser	Cys	Gln	Phe	Thr	Thr	Asp	Leu	Ile	Ala	Met	Asn	His	Ala	Asp	Phe		
						470				475					480		
Ile	Ile	Thr	Ser	Thr	Phe	Gln	Glu	Ile	Ala	Gly	Asn	Lys	Asp	Thr	Val		
					485					490					495		
Gly	Gln	Tyr	Glu	Ser	His	Met	Ala	Phe	Thr	Met	Pro	Gly	Leu	Tyr	Arg		
			500					505						510			
Val	Val	His	Gly	Ile	Asp	Val	Phe	Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser		
		515					520						525				
Pro	Gly	Ala	Asp	Leu	Ser	Ile	Tyr	Phe	Pro	Tyr	Thr	Glu	Ser	His	Lys		
		530					535					540					
Arg	Leu	Thr	Ser	Leu	His	Pro	Glu	Ile	Glu	Glu	Leu	Leu	Tyr	Ser	Gln		
					550					555					560		
Thr	Glu	Asn	Thr	Glu	His	Lys	Phe	Val	Leu	Asn	Asp	Arg	Asn	Lys	Pro		
					565					570					575		
Ile	Ile	Phe	Ser	Met	Ala	Arg	Leu	Asp	Arg	Val	Lys	Asn	Leu	Thr	Gly		
					580				585					590			
Leu	Val	Glu	Leu	Tyr	Gly	Arg	Asn	Lys	Arg	Leu	Gln	Glu	Leu	Val	Asn		
		595					600					605					
Leu	Val	Val	Val	Cys	Gly	Asp	His	Gly	Asn	Pro	Ser	Lys	Asp	Lys	Glu		
		610				615					620						
Glu	Gln	Ala	Glu	Phe	Lys	Lys	Met	Phe	Asp	Leu	Ile	Glu	Gln	Tyr	Asn		
					630				635						640		
Leu	Asn	Gly	His	Ile	Arg	Trp	Ile	Ser	Ala	Gln	Met	Asn	Arg	Val	Arg		
					645				650						655		
Asn	Gly	Glu	Leu	Tyr	Arg	Tyr	Ile	Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val		
			660					665						670			
Gln	Pro	Ala	Phe	Tyr	Glu	Ala	Phe	Gly	Leu	Thr	Val	Val	Glu	Ala	Met		
		675					680						685				
Thr	Cys	Gly	Leu	Pro	Thr	Phe	Ala	Thr	Ala	Tyr	Gly	Gly	Pro	Ala	Glu		
		690				695						700					
Ile	Ile	Val	His	Gly	Val	Ser	Gly	Tyr	His	Ile	Asp	Pro	Tyr	Gln	Gly		
					710					715					720		
Asp	Lys	Ala	Ser	Ala	Leu	Leu	Val	Asp	Phe	Phe	Asp	Lys	Cys	Gln	Ala		
					725				730					735			
Glu	Pro	Ser	His	Trp	Ser	Lys	Ile	Ser	Gln	Gly	Gly	Leu	Gln	Arg	Ile		
					740				745					750			
Glu	Glu	Lys	Tyr	Thr	Trp	Lys	Leu	Tyr	Ser	Glu	Arg	Leu	Met	Thr	Leu		
		755					760						765				
Thr	Gly	Val	Tyr	Gly	Phe	Trp	Lys	Tyr	Val	Ser	Asn	Leu	Glu	Arg	Arg		
		770				775					780						
Glu	Thr	Arg	Arg	Tyr	Leu	Glu	Met	Leu	Tyr	Ala	Leu	Lys	Tyr	Arg	Thr		
					790					795					800		
Met	Ala	Ser	Thr	Val	Pro	Leu	Ala	Val	Glu	Gly	Glu	Pro	Ser	Ser	Lys		
					805				810						815		

<210> 8
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 8
 acggaatcgt tcgcaagtgg atctc

```

<210> 9
<211> 25
<212> DNA
<213> Zea mays

<400> 9
gatgattggc ttgttcctgt cgttc
25

<210> 10
<211> 32
<212> DNA
<213> Zea mays

<400> 10
agagaagcca acgccawcgc ctcyatttcg tc
32

<210> 11
<211> 2757
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(2430)

<221> source
<222> (1)...(39)
<223> Sorghum propinquum

<221> source
<222> (39)...(2757)
<223> Zea mays

<223> synthetic sequence

<400> 11
atg tct gcc ccg aag ctg aac cgc aac gcg agc atc cgg gac cgc gtc 48
Met Ser Ala Pro Lys Leu Asn Arg Asn Ala Ser Ile Arg Asp Arg Val
1 5 10 15

gag gac acc ctc cac gcg cac cgc aac gag ctc gtc gcc ctc ctc tcc 96
Glu Asp Thr Leu His Ala His Arg Asn Glu Leu Val Ala Leu Leu Ser
20 25 30

aag tac gtg aac aag ggg aag ggc atc ctg cag ccg cac cac atc ctc 144
Lys Tyr Val Asn Lys Gly Lys Gly Ile Leu Gln Pro His His Ile Leu
35 40 45

gac gcg ctc gac gag gtc cag ggc tcc ggg gtc cgc gcg ctc gcc gag 192
Asp Ala Leu Asp Glu Val Gln Gly Ser Gly Val Arg Ala Leu Ala Glu
50 55 60

gga ccc ttc ctc gac gtc ctc cgc tcc gcg cag gag gcg atc gtg ctg 240
Gly Pro Phe Leu Asp Val Leu Arg Ser Ala Gln Glu Ala Ile Val Leu
65 70 75 80

ccg ccg ttc gtg gcc atc gcg gtg cgc ccg cgc ccg gga gtt tgg gag 288
Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu

```


	85	90	95	
tac gtc cgc gtc aac gtt cac gag ctc agc gtc gag cag ctc aca gtc				336
Tyr Val Arg Val Asn Val His Glu Leu Ser Val Glu Gln Leu Thr Val				
	100	105	110	
tcg gag tac ctc cgc ttc aag gag gag ctt gtc gac ggc cag cac aat				384
Ser Glu Tyr Leu Arg Phe Lys Glu Glu Leu Val Asp Gly Gln His Asn				
	115	120	125	
gat ccc tac gtt ctc gag ctt gac ttc gag ccg ttc aat gtc tca gtc				432
Asp Pro Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Val Ser Val				
	130	135	140	
cca cgc cca aat cgg tca tca tct att gga aac ggt gtg cag ttc ctc				480
Pro Arg Pro Asn Arg Ser Ser Ser Ile Gly Asn Gly Val Gln Phe Leu				
	145	150	155	160
aac cga cac ttg tcc tca atc atg ttc cgc aac agg gat tgc ttg gag				528
Asn Arg His Leu Ser Ser Ile Met Phe Arg Asn Arg Asp Cys Leu Glu				
	165	170	175	
ccc ctg ttg gat ttc ctc cgt ggc cac cgg cac aag ggg cat gtt atg				576
Pro Leu Leu Asp Phe Leu Arg Gly His Arg His Lys Gly His Val Met				
	180	185	190	
atg ctt aat gat aga ata caa agc ttg ggg agg ctt cag tct gtg ctg				624
Met Leu Asn Asp Arg Ile Gln Ser Leu Gly Arg Leu Gln Ser Val Leu				
	195	200	205	
acc aaa gct gag gag cac ttg tca aag ctc cct gct gac aca cca tac				672
Thr Lys Ala Glu Glu His Leu Ser Lys Leu Pro Ala Asp Thr Pro Tyr				
	210	215	220	
tca caa ttt gct tat aaa ttt caa gag tgg ggc ctg gag aaa ggt tgg				720
Ser Gln Phe Ala Tyr Lys Phe Gln Glu Trp Gly Leu Glu Lys Gly Trp				
	225	230	235	240
ggg gat aca gca gga cat gtt ttg gaa atg atc cat ctc ctt cta gac				768
Gly Asp Thr Ala Gly His Val Leu Glu Met Ile His Leu Leu Leu Asp				
	245	250	255	
atc att cag gcg cca gac cca tct acc cta gag aaa ttc ttg ggg agg				816
Ile Ile Gln Ala Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Arg				
	260	265	270	
atc ccc atg att ttt aac gtt gtt gtg gta tcc cct cat gga tac ttt				864
Ile Pro Met Ile Phe Asn Val Val Val Ser Pro His Gly Tyr Phe				
	275	280	285	
ggg caa gct aat gta tta ggc ttg cca gac aca gga gga cag atc gtc				912
Gly Gln Ala Asn Val Leu Gly Leu Pro Asp Thr Gly Gly Gln Ile Val				
	290	295	300	
tat ata ctg gac caa gtc cgt gca cta gaa aat gag atg gtt ctc cgt				960
Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Val Leu Arg				
	305	310	315	320

tta aag aaa caa ggg ctt gat gtt tcc cca aag att ctc att gtt act	1008
Leu Lys Lys Gln Gly Leu Asp Val Ser Pro Lys Ile Leu Ile Val Thr	
325 330 335	
cgg ctg ata cca gat gca aaa gga aca tca tgc aat cag cgg ctt gag	1056
Arg Leu Ile Pro Asp Ala Lys Gly Thr Ser Cys Asn Gln Arg Leu Glu	
340 345 350	
aga att agt gga aca cag cat act tac ata tta cga gtt ccc ttc aga	1104
Arg Ile Ser Gly Thr Gln His Thr Tyr Ile Leu Arg Val Pro Phe Arg	
355 360 365	
aat gaa aat ggg ata ctt aag aaa tgg ata tca aga ttt gat gtg tgg	1152
Asn Glu Asn Gly Ile Leu Lys Lys Trp Ile Ser Arg Phe Asp Val Trp	
370 375 380	
cca tat ctg gaa aca ttt gct gag gat gct gct ggt gaa att gct gct	1200
Pro Tyr Leu Glu Thr Phe Ala Glu Asp Ala Ala Gly Glu Ile Ala Ala	
385 390 395 400	
gaa tta caa ggt act cca gac ttc ata att gga aac tac agt gat gga	1248
Glu Leu Gln Gly Thr Pro Asp Phe Ile Ile Gly Asn Tyr Ser Asp Gly	
405 410 415	
aat ctt gtg gcg tca ttg cta tct tac aag atg gga att acc cag tgc	1296
Asn Leu Val Ala Ser Leu Leu Ser Tyr Lys Met Gly Ile Thr Gln Cys	
420 425 430	
aac att gct cat gct ctg gaa aag act aag tat cca gat tca gac ata	1344
Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile	
435 440 445	
ttt tgg aag aat ttc gat gag aag tac cat ttc tcc tgc cag ttc act	1392
Phe Trp Lys Asn Phe Asp Glu Lys Tyr His Phe Ser Cys Gln Phe Thr	
450 455 460	
gct gat ata att gct atg aac aat gct gat ttt atc atc acc agc aca	1440
Ala Asp Ile Ile Ala Met Asn Asn Ala Asp Phe Ile Ile Thr Ser Thr	
465 470 475 480	
tac caa gaa att gct gga agc aaa aat act gtt gga cag tat gag agt	1488
Tyr Gln Glu Ile Ala Gly Ser Lys Asn Thr Val Gly Gln Tyr Glu Ser	
485 490 495	
cat act gcc ttt act ctg cct ggt ctg tac cga gtt gtc cat ggg atc	1536
His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile	
500 505 510	
gat gtc ttc gat cca aag ttc aat ata gtc tct cct gga gct gac atg	1584
Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met	
515 520 525	
tcc ata tac ttt cca cat acc gag aag gcc aag cga ctc acc tct ctt	1632
Ser Ile Tyr Phe Pro His Thr Glu Lys Ala Lys Arg Leu Thr Ser Leu	
530 535 540	
cat ggt tca atc gaa aat ttg att tat gac ccg gag caa aac gat gaa	1680
His Gly Ser Ile Glu Asn Leu Ile Tyr Asp Pro Glu Gln Asn Asp Glu	

545	550	555	560	
cac att ggg cat ctg gat gac cgg tca aag ccc atc ctc ttc tcc atg				1728
His Ile Gly His Leu Asp Asp Arg Ser Lys Pro Ile Leu Phe Ser Met				
	565	570	575	
gca aga ctc gac agg gtg aag aac ata aca ggg ctg gtc gaa gct ttt				1776
Ala Arg Leu Asp Arg Val Lys Asn Ile Thr Gly Leu Val Glu Ala Phe				
	580	585	590	
gct aag tgc gct aag ctg agg gag ctg gta aac ctt gtc gtc gtt gcc				1824
Ala Lys Cys Ala Lys Leu Arg Glu Leu Val Asn Leu Val Val Val Ala				
	595	600	605	
ggg tac aat gat gtc aac aag tcc aag gac agg gaa gag atc gcg gag				1872
Gly Tyr Asn Asp Val Asn Lys Ser Lys Asp Arg Glu Glu Ile Ala Glu				
	610	615	620	
ata gag aag atg cat gaa ctc atc aag acc cac aac ttg ttc ggg cag				1920
Ile Glu Lys Met His Glu Leu Ile Lys Thr His Asn Leu Phe Gly Gln				
	625	630	635	640
ttc cgc tgg atc tct gcc cag aca aac agg gcc cgt aac ggc gag ctc				1968
Phe Arg Trp Ile Ser Ala Gln Thr Asn Arg Ala Arg Asn Gly Glu Leu				
	645	650	655	
tat cgc tac atc gct gat acc cat ggt gct ttc gta cag ccg gcc ttg				2016
Tyr Arg Tyr Ile Ala Asp Thr His Gly Ala Phe Val Gln Pro Ala Leu				
	660	665	670	
tat gaa gcg ttc ggt ctc acc gtc gtt gag gcc atg acc tgt ggg ctt				2064
Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu				
	675	680	685	
cct act ttc gcg acg ctc cat gga ggt cca gct gag atc ata gag cat				2112
Pro Thr Phe Ala Thr Leu His Gly Gly Pro Ala Glu Ile Ile Glu His				
	690	695	700	
ggc gtc tcg ggc ttc cac att gac ccg tac cac ccc gaa cag gct gtt				2160
Gly Val Ser Gly Phe His Ile Asp Pro Tyr His Pro Glu Gln Ala Val				
	705	710	715	720
aat ctg atg gcc gac ttc ttc gac cgg tgc aag caa gac cca gat cac				2208
Asn Leu Met Ala Asp Phe Phe Asp Arg Cys Lys Gln Asp Pro Asp His				
	725	730	735	
tgg gtg aat ata tct gga gca ggg ctg cag cgc ata tac gag aag tac				2256
Trp Val Asn Ile Ser Gly Ala Gly Leu Gln Arg Ile Tyr Glu Lys Tyr				
	740	745	750	
aca tgg aag ata tac tca gag agg ttg atg aca ctg gcc ggg gtc tac				2304
Thr Trp Lys Ile Tyr Ser Glu Arg Leu Met Thr Leu Ala Gly Val Tyr				
	755	760	765	
ggt ttc tgg aag tac gtg tcg aag ctc gag agg ctg gag acg agg cgc				2352
Gly Phe Trp Lys Tyr Val Ser Lys Leu Glu Arg Leu Glu Thr Arg Arg				
	770	775	780	

tac ctt gag atg ttc tac ata ctg aag ttc cgc gag ctg gcg aag acc 2400
Tyr Leu Glu Met Phe Tyr Ile Leu Lys Phe Arg Glu Leu Ala Lys Thr
785 790 795 800

gtg ccg ctt gca att gac caa ccg cag tag cttgcgcaac tgcgactgcg 2450
Val Pro Leu Ala Ile Asp Gln Pro Gln *
805

tagcacttgg tacaagactg aaacctgaag gaccttcagt aatttaggcg cggcagacgg 2510
tagccaataa aatgtgccgg agctgaactg gttttttatt atgtacataa tggcagtata 2570
acaaaattac tgaaggcagg tgggttgacg ttgtgtgttc gttactgttt actgtattat 2630
gtcaagctgt cggctgcaat ttctttgctg gcaagccgca ggcactggtg aagtgcgat 2690
aaatacatca tattctgttg acctgtgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaggg 2750
cgccgc 2757

<210> 12

<211> 809

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 12

Met	Ser	Ala	Pro	Lys	Leu	Asn	Arg	Asn	Ala	Ser	Ile	Arg	Asp	Arg	Val
1				5				10					15		
Glu	Asp	Thr	Leu	His	Ala	His	Arg	Asn	Glu	Leu	Val	Ala	Leu	Leu	Ser
			20					25					30		
Lys	Tyr	Val	Asn	Lys	Gly	Lys	Gly	Ile	Leu	Gln	Pro	His	His	Ile	Leu
			35				40					45			
Asp	Ala	Leu	Asp	Glu	Val	Gln	Gly	Ser	Gly	Val	Arg	Ala	Leu	Ala	Glu
			50			55				60					
Gly	Pro	Phe	Leu	Asp	Val	Leu	Arg	Ser	Ala	Gln	Glu	Ala	Ile	Val	Leu
					70					75					80
Pro	Pro	Phe	Val	Ala	Ile	Ala	Val	Arg	Pro	Arg	Pro	Gly	Val	Trp	Glu
				85				90						95	
Tyr	Val	Arg	Val	Asn	Val	His	Glu	Leu	Ser	Val	Glu	Gln	Leu	Thr	Val
			100					105					110		
Ser	Glu	Tyr	Leu	Arg	Phe	Lys	Glu	Glu	Leu	Val	Asp	Gly	Gln	His	Asn
			115				120				125				
Asp	Pro	Tyr	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Val	Ser	Val
			130			135					140				
Pro	Arg	Pro	Asn	Arg	Ser	Ser	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu
					150					155					160
Asn	Arg	His	Leu	Ser	Ser	Ile	Met	Phe	Arg	Asn	Arg	Asp	Cys	Leu	Glu
			165					170						175	
Pro	Leu	Leu	Asp	Phe	Leu	Arg	Gly	His	Arg	His	Lys	Gly	His	Val	Met
			180				185						190		
Met	Leu	Asn	Asp	Arg	Ile	Gln	Ser	Leu	Gly	Arg	Leu	Gln	Ser	Val	Leu
			195				200					205			
Thr	Lys	Ala	Glu	Glu	His	Leu	Ser	Lys	Leu	Pro	Ala	Asp	Thr	Pro	Tyr
			210			215					220				
Ser	Gln	Phe	Ala	Tyr	Lys	Phe	Gln	Glu	Trp	Gly	Leu	Glu	Lys	Gly	Trp
					230					235					240
Gly	Asp	Thr	Ala	Gly	His	Val	Leu	Glu	Met	Ile	His	Leu	Leu	Leu	Asp
				245					250					255	
Ile	Ile	Gln	Ala	Pro	Asp	Pro	Ser	Thr	Leu	Glu	Lys	Phe	Leu	Gly	Arg
			260					265						270	

10080114.022102

Ile	Pro	Met	Ile	Phe	Asn	Val	Val	Val	Val	Ser	Pro	His	Gly	Tyr	Phe
		275						280				285			
Gly	Gln	Ala	Asn	Val	Leu	Gly	Leu	Pro	Asp	Thr	Gly	Gly	Gln	Ile	Val
		290					295					300			
Tyr	Ile	Leu	Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Val	Leu	Arg
305					310					315					320
Leu	Lys	Lys	Gln	Gly	Leu	Asp	Val	Ser	Pro	Lys	Ile	Leu	Ile	Val	Thr
				325						330					335
Arg	Leu	Ile	Pro	Asp	Ala	Lys	Gly	Thr	Ser	Cys	Asn	Gln	Arg	Leu	Glu
			340						345						350
Arg	Ile	Ser	Gly	Thr	Gln	His	Thr	Tyr	Ile	Leu	Arg	Val	Pro	Phe	Arg
		355						360					365		
Asn	Glu	Asn	Gly	Ile	Leu	Lys	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp
		370					375					380			
Pro	Tyr	Leu	Glu	Thr	Phe	Ala	Glu	Asp	Ala	Ala	Gly	Glu	Ile	Ala	Ala
385					390					395					400
Glu	Leu	Gln	Gly	Thr	Pro	Asp	Phe	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly
				405						410					415
Asn	Leu	Val	Ala	Ser	Leu	Leu	Ser	Tyr	Lys	Met	Gly	Ile	Thr	Gln	Cys
			420						425						430
Asn	Ile	Ala	His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr	Pro	Asp	Ser	Asp	Ile
		435						440							445
Phe	Trp	Lys	Asn	Phe	Asp	Glu	Lys	Tyr	His	Phe	Ser	Cys	Gln	Phe	Thr
		450					455					460			
Ala	Asp	Ile	Ile	Ala	Met	Asn	Asn	Ala	Asp	Phe	Ile	Ile	Thr	Ser	Thr
465					470					475					480
Tyr	Gln	Glu	Ile	Ala	Gly	Ser	Lys	Asn	Thr	Val	Gly	Gln	Tyr	Glu	Ser
				485						490					495
His	Thr	Ala	Phe	Thr	Leu	Pro	Gly	Leu	Tyr	Arg	Val	Val	His	Gly	Ile
			500						505						510
Asp	Val	Phe	Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met
		515						520					525		
Ser	Ile	Tyr	Phe	Pro	His	Thr	Glu	Lys	Ala	Lys	Arg	Leu	Thr	Ser	Leu
		530						535							540
His	Gly	Ser	Ile	Glu	Asn	Leu	Ile	Tyr	Asp	Pro	Glu	Gln	Asn	Asp	Glu
545					550					555					560
His	Ile	Gly	His	Leu	Asp	Asp	Arg	Ser	Lys	Pro	Ile	Leu	Phe	Ser	Met
				565						570					575
Ala	Arg	Leu	Asp	Arg	Val	Lys	Asn	Ile	Thr	Gly	Leu	Val	Glu	Ala	Phe
				580					585						590
Ala	Lys	Cys	Ala	Lys	Leu	Arg	Glu	Leu	Val	Asn	Leu	Val	Val	Val	Ala
		595						600							605
Gly	Tyr	Asn	Asp	Val	Asn	Lys	Ser	Lys	Asp	Arg	Glu	Glu	Ile	Ala	Glu
		610					615								620
Ile	Glu	Lys	Met	His	Glu	Leu	Ile	Lys	Thr	His	Asn	Leu	Phe	Gly	Gln
625					630					635					640
Phe	Arg	Trp	Ile	Ser	Ala	Gln	Thr	Asn	Arg	Ala	Arg	Asn	Gly	Glu	Leu
				645						650					655
Tyr	Arg	Tyr	Ile	Ala	Asp	Thr	His	Gly	Ala	Phe	Val	Gln	Pro	Ala	Leu
			660						665						670
Tyr	Glu	Ala	Phe	Gly	Leu	Thr	Val	Val	Glu	Ala	Met	Thr	Cys	Gly	Leu
		675						680							685
Pro	Thr	Phe	Ala	Thr	Leu	His	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Glu	His
		690					695								700
Gly	Val	Ser	Gly	Phe	His	Ile	Asp	Pro	Tyr	His	Pro	Glu	Gln	Ala	Val
705					710					715					720
Asn	Leu	Met	Ala	Asp	Phe	Phe	Asp	Arg	Cys	Lys	Gln	Asp	Pro	Asp	His
				725						730					735

10060114-022102

Trp	Val	Asn	Ile	Ser	Gly	Ala	Gly	Leu	Gln	Arg	Ile	Tyr	Glu	Lys	Tyr
		740						745					750		
Thr	Trp	Lys	Ile	Tyr	Ser	Glu	Arg	Leu	Met	Thr	Leu	Ala	Gly	Val	Tyr
		755						760					765		
Gly	Phe	Trp	Lys	Tyr	Val	Ser	Lys	Leu	Glu	Arg	Leu	Glu	Thr	Arg	Arg
		770						775					780		
Tyr	Leu	Glu	Met	Phe	Tyr	Ile	Leu	Lys	Phe	Arg	Glu	Leu	Ala	Lys	Thr
		785				790				795					800
Val	Pro	Leu	Ala	Ile	Asp	Gln	Pro	Gln							
				805											

<210> 13
 <211> 347
 <212> DNA
 <213> Sorghum propinquum

<400> 13
 cgccagtcgc cagtcgccac agccacacca caccacacta gccgcggccg cgggtaggag 60
 cgcgcgcggc gcggcggaac gacccaccgg tggcggcagc catgtctgcc ccgaagctga 120
 accgcaacgc gagcatccgg gaccgcgtcg aggacaccct ccacgcgcac cgcaacgagc 180
 tcgtcgccct cctctccaag tacgtgaaca aggggaaggg catcctgcag ccgcaccaca 240
 tcctcgacgc gctcgacgag gtccagggtc ccgggggtccg cgcgctcgcc gagggaccct 300
 tcctcgacgt cctccgctcc gcgcaggagg cgatcggtgt gccgccg 347

1008044.023402